Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

Please cancel claims1- 43 and add following new claims:

44. (New) A method for quantifying one or more peptides in a peptide mixture, comprising:

receiving a first peptide mixture containing a plurality of peptides;

separating one or more of the plurality of peptides of the first peptide mixture over a period of time;

mass-to-charge analyzing one or more of the separated peptides of the first peptide mixture at a particular time in the period of time;

calculating an abundance of one or more of the mass analyzed peptides of the first peptide mixture; and

calculating a relative quantity for the one or more mass analyzed peptides of the first peptide mixture by comparing the calculated abundance of the one or more mass analyzed peptides of the first peptide mixture with an abundance of one or more peptides in a reference sample, the reference sample being external to the first peptide mixture.

45. (New) The method of claim 44, wherein:

receiving a first peptide mixture containing a plurality of peptides comprises digesting a first polypeptide sample to generate the first peptide mixture.

46. (New) The method of claim 45, further comprising:

preparing the reference sample by digesting a second polypeptide sample;

separating one or more peptides from the digested second polypeptide sample;

mass analyzing the separated peptides from the digested second polypeptide sample; and

calculating an abundance of one or more of the mass analyzed peptides from the second polypeptide sample;

wherein calculating a relative quantity for the one or more mass analyzed peptides of the first peptide mixture comprises comparing the calculated abundance of the one or more mass analyzed peptides of the first peptide mixture with the calculated abundance of one or more corresponding mass analyzed peptides from the second polypeptide sample.

47. (New) The method of claim 44, wherein:

separating one or more peptides comprises separating the one or more peptides by liquid chromatography.

48. (New) The method of claim 47, wherein:

separating one or more peptides comprises isolating a liquid chromatography eluent at the particular time; and

mass analyzing one or more of the separated peptides of the first peptide mixture comprises mass analyzing one or more peptides in the isolated eluent.

49. (New) The method of claim 44, further comprising:

identifying one or more peptides of the first peptide mixture.

50. (New) The method of claim 49, wherein:

identifying one or more peptides of the first peptide mixture comprises identifying one or more of the separated peptides based on mass analysis information.

51. (New) The method of claim 50, wherein:

mass analyzing one or more of the separated peptides comprises fragmenting an ion derived from a peptide of the one or more separated peptides and mass analyzing fragments of the ion; and

identifying one or more peptides in the first sample comprises searching a sequence database based on mass analysis information for the fragments.

52. (New) The method of claim 47, wherein:

calculating an abundance of one or more of the mass analyzed peptides comprises reconstructing a chromatogram peak for a peptide based on mass analysis information for the peptide.

53. (New) The method of claim 52, wherein:

calculating an abundance for a peptide comprises calculating an abundance for a peptide based on a reconstructed chromatogram peak area for the peptide.

54. (New) The method of claim 53, wherein:

calculating the abundance for a peptide comprises calculating an abundance for a peptide using only chromatogram peaks located within a threshold distance in the reconstructed chromatogram of the particular time.

55. (New) The method of claim 53, wherein:

calculating a relative quantity for the one or more mass analyzed peptides comprises comparing an abundance calculated by reconstructing a chromatogram peak area for a peptide of the first peptide mixture with an abundance calculated by reconstructing a chromatogram peak area for a peptide in the reference sample.

56. (New) The method of claim 45, further comprising:

normalizing the calculated abundance of the one or more mass analyzed peptides of the first peptide mixture.

57. (New) The method of claim 56, wherein:

normalizing the calculated abundance comprises normalizing the calculated abundance based on an internal standard including one or more peptides added to the first polypeptide sample.

58. (New) The method of claim 56, wherein:

normalizing the calculated abundance comprises normalizing the calculated abundance based on an external standard including one or more peptides.

59. (New) The method of claim 45, further comprising:

identifying a plurality of peptides of the first peptide mixture based on the mass analyzing;

wherein calculating a relative quantity for the one or more mass analyzed peptides comprises calculating a relative quantity for each of the identified peptides.

60. (New) The method of claim 59, further comprising:

normalizing calculated abundances for each of the identified peptides by calculating a correction factor based on reconstructed chromatogram peak areas for a set of peptides in the first peptide mixture, each peptide in the set of peptides having constant chromatogram peak areas over a plurality of experiments, and applying the correction factor to the calculated abundance for each of the identified peptides.

61. (New) The method of claim 44, wherein:

mass-to-charge analyzing one or more of the separated peptides and calculating an abundance of one or more of the mass analyzed peptides comprises mass-to-charge analyzing and calculating an abundance for one or more arbitrary peptides of the first peptide mixture.

62. (New) A method of quantifying one or more peptides in a mixture, comprising:

digesting a protein sample to generate a mixture of peptides;

separating one or more peptides of the mixture of peptides using liquid chromatography;

mass analyzing one or more of the separated peptides;

identifying one or more of the mass analyzed peptides based on mass spectra for the peptides;

calculating chromatogram peak areas for the identified peptides;

calculating chromatogram peak areas for one or more proteins corresponding to the identified peptides based on the calculated peak areas for the corresponding peptides;

normalizing the chromatogram peak area for the protein based on a chromatogram peak area for an internal standard; and

determining a relative quantity for a protein of the one or more of the proteins by comparing the normalized chromatogram peak area for the protein to a chromatogram peak area for a corresponding protein in a reference sample.

63. (New) An apparatus for quantifying one or more peptides in a peptide mixture, comprising:

means for receiving a first peptide mixture containing a plurality of peptides;

means for separating one or more of the plurality of peptides of the first peptide mixture over a period of time;

means for mass analyzing one or more of the separated peptides of the first peptide mixture at a particular time in the period of time;

means for calculating an abundance of one or more of the mass analyzed peptides of the first peptide mixture;

means for calculating a relative quantity for the one or more mass analyzed peptides of the first peptide mixture by comparing the calculated abundance of the one or more mass analyzed peptides of the first peptide mixture with an abundance of one or more peptides in a reference sample which is external to first peptide mixture.

64. (New) The apparatus of claim 63, further comprising:

means for receiving at least one additional peptide mixture.

65. (New) The apparatus of claim 64, wherein:

the at least one additional peptide mixture comprises a reference sample.

66. (New) The apparatus of claim 63, wherein:

the means for calculating an abundance further comprises reference information.

67. (New) The apparatus of claim 63, wherein:

the means for mass-to-charge analyzing and the means for calculating are configured to mass-to-charge analyze and calculate an abundance for one or more arbitrary peptides of the first peptide mixture.

68. (New) The apparatus of claim 63, wherein:

the means for separating, mass-to-charge analyzing, and calculating steps are configured to separate, mass-to-charge analyze and calculate an abundance for one or more peptides independent of a particular amino acid composition of the subject peptides.

69. (New) A computer program product on a computer-readable medium for quantifying one or more peptides in a first peptide mixture, the product comprising instructions operable to cause a programmable processor to:

receive separation information representing a separation of one or more of a plurality of peptides of a first peptide mixture over a period of time;

receive mass-to-charge analysis information for one or more of the separated peptides of the first peptide mixture at a particular time in the period of time;

calculate an abundance of one or more of the mass analyzed peptides of the first peptide mixture; and

calculate a relative quantity for the one or more mass analyzed peptides of the first peptide mixture by comparing the calculated abundance of the one or more mass analyzed peptides of the first peptide mixture with an abundance of one or more peptides in a reference sample, the reference sample being external to the first peptide mixture.

70. (New) A computer program product on a computer-readable medium for quantifying one or more peptides in a first peptide mixture, the product comprising instructions operable to cause a programmable processor to:

receive separation information representing a separation of one or more of a plurality of peptides of a first peptide mixture over a period of time;

receive mass-to-charge analysis information for one or more of the separated peptides of the first peptide mixture at a particular time in the period of time;

identify one or more of the mass analyzed peptides based on the mass-to-charge analysis information for the peptides;

calculate chromatogram peak areas for the identified peptides;

calculate chromatogram peak areas for one or more proteins corresponding to the identified peptides based on the calculated peak areas for the corresponding peptides;

normalize the chromatogram peak area for the protein based on a chromatogram peak area for an internal standard; and

determine a relative quantity for a protein of the one or more of the proteins by comparing the normalized chromatogram peak area for the protein to a chromatogram peak area for a corresponding protein in a reference sample.

71. (New) Apparatus for quantifying one or more peptides in a first peptide mixture, the apparatus comprising digital circuitry configured to perform the following actions:

receive separation information representing a separation of one or more of a plurality of peptides of a first peptide mixture over a period of time;

receive mass-to-charge analysis information for one or more of the separated peptides of the first peptide mixture at a particular time in the period of time;

calculate an abundance of one or more of the mass analyzed peptides of the first peptide mixture; and

calculate a relative quantity for the one or more mass analyzed peptides of the first peptide mixture by comparing the calculated abundance of the one or more mass analyzed peptides of the first peptide mixture with an abundance of one or more peptides in a reference sample, the reference sample being external to the first peptide mixture.

72. (New) Apparatus for quantifying one or more peptides in a first peptide mixture, the apparatus comprising digital circuitry configured to perform the following actions:

receive separation information representing a separation of one or more of a plurality of peptides of a first peptide mixture over a period of time;

receive mass-to-charge analysis information for one or more of the separated peptides of the first peptide mixture at a particular time in the period of time;

identify one or more of the mass analyzed peptides based on the mass-to-charge analysis information for the peptides;

calculate chromatogram peak areas for the identified peptides;

calculate chromatogram peak areas for one or more proteins corresponding to the identified peptides based on the calculated peak areas for the corresponding peptides;

normalize the chromatogram peak area for the protein based on a chromatogram peak area for an internal standard; and

determine a relative quantity for a protein of the one or more of the proteins by comparing the normalized chromatogram peak area for the protein to a chromatogram peak area for a corresponding protein in a reference sample.

73. (New) A method for quantifying one or more compounds in a biological sample, comprising:

receiving a biological sample containing a plurality of compounds;

separating one or more of the plurality of compounds of the biological sample over a period of time;

mass-to-charge analyzing one or more of the separated compounds of the biological sample at a particular time in the period of time;

calculating an abundance of one or more of the mass analyzed compounds of the biological sample; and

calculating a relative quantity for the one or more mass analyzed compounds of the biological sample by comparing the calculated abundance of the one or more mass analyzed compounds of the biological sample with an abundance of one or more compounds in a reference sample, the reference sample being external to the biological sample.

74. (New) Apparatus for quantifying one or more compounds in a biological sample, the apparatus comprising digital circuitry configured to perform the following actions:

receive a biological sample containing a plurality of compounds;

separate one or more of the plurality of compounds of the biological sample over a period of time;

mass-to-charge analyze one or more of the separated compounds of the biological sample at a particular time in the period of time;

calculate an abundance of one or more of the mass analyzed compounds of the biological sample; and

calculate a relative quantity for the one or more mass analyzed compounds of the biological sample by comparing the calculated abundance of the one or more mass analyzed compounds of the biological sample with an abundance of one or more compounds in a reference sample, the reference sample being external to the biological sample.